

RAW SEQUENCE LISTING

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Application Serial Number: 09/619,310C
Source: IFW/6
Date Processed by STIC: 3/8/05

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IFW16

RAW SEQUENCE LISTING

DATE: 03/08/2005

PATENT APPLICATION: US/09/619,310C

TIME: 10:36:33

Input Set : A:\2005-01-02 4614-0140PUS1.ST25.txt

Output Set: N:\CRF4\03082005\I619310C.raw

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3 <110> APPLICANT: THASTRUP, Ole
4     TULLIN, Soren
5     POULSEN, Lars K
6     BJORN, Sara P
8 <120> TITLE OF INVENTION: NOVEL FLUORESCENT PROTEINS
10 <130> FILE REFERENCE: 4614-0140PUS1
12 <140> CURRENT APPLICATION NUMBER: US 09/619,310C
13 <141> CURRENT FILING DATE: 2000-07-19
15 <150> PRIOR APPLICATION NUMBER: US 08/819,612
16 <151> PRIOR FILING DATE: 1997-03-17
18 <150> PRIOR APPLICATION NUMBER: PCT/DK96/00051
19 <151> PRIOR FILING DATE: 1996-01-31
21 <150> PRIOR APPLICATION NUMBER: DK 1065/95
22 <151> PRIOR FILING DATE: 1995-09-22
25 <160> NUMBER OF SEQ ID NOS: 23
27 <170> SOFTWARE: PatentIn version 3.2
29 <210> SEQ ID NO: 1
30 <211> LENGTH: 36
31 <212> TYPE: DNA
32 <213> ORGANISM: Artificial Sequence
34 <220> FEATURE:
35 <223> OTHER INFORMATION: GFP2 primer directed to A. victoria
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46 <220> FEATURE:
47 <223> OTHER INFORMATION: GFP-1 primer directed to A. victoria
49 <400> SEQUENCE: 2
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53 <210> SEQ ID NO: 3
54 <211> LENGTH: 67
55 <212> TYPE: DNA
56 <213> ORGANISM: Artificial Sequence
58 <220> FEATURE:
59 <223> OTHER INFORMATION: 5' PCR primer incorporating the Y66H substitution responsible
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60     changing green fluorescence into blue fluorescence
62 <400> SEQUENCE: 3
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65 gataccc          67
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69 <211> LENGTH: 36
 70 <212> TYPE: DNA
 71 <213> ORGANISM: Artificial Sequence
 73 <220> FEATURE:
 74 <223> OTHER INFORMATION: 3' PCR primer incorporating the Y66H substitution responsible
 for
 75 changing green fluorescence into blue fluorescence
 77 <400> SEQUENCE: 4
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 82 <211> LENGTH: 30
 83 <212> TYPE: DNA
 84 <213> ORGANISM: Artificial Sequence
 86 <220> FEATURE:
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 90 aattggtacc aaggaggtaa gctttatgag 30
 93 <210> SEQ ID NO: 6
 94 <211> LENGTH: 30
 95 <212> TYPE: DNA
 96 <213> ORGANISM: Artificial Sequence
 98 <220> FEATURE:
 99 <223> OTHER INFORMATION: 3' primer used to flank the Y66H-GFP
 101 <400> SEQUENCE: 6
 102 ctttcgtttt gaattcggat cccttttagtg 30
 105 <210> SEQ ID NO: 7
 106 <211> LENGTH: 48
 107 <212> TYPE: DNA
 108 <213> ORGANISM: Artificial Sequence
 110 <220> FEATURE:
 111 <223> OTHER INFORMATION: large NcoI-XbaI vector fragment and ligated to SEQ ID NO:8
 113 <400> SEQUENCE: 7
 114 catggccaac gcttgctcact actctctctt atggtgttca atgctttt 48
 117 <210> SEQ ID NO: 8
 118 <211> LENGTH: 48
 119 <212> TYPE: DNA
 120 <213> ORGANISM: Artificial Sequence
 122 <220> FEATURE:
 123 <223> OTHER INFORMATION: synthetic NcoI-XbaI DNA linker and ligated to SEQ ID NO:7
 125 <400> SEQUENCE: 8
 126 ctagaaaagc attgaacacc ataagagaga gtagtgacaa gcgttggc 48
 129 <210> SEQ ID NO: 9
 130 <211> LENGTH: 48
 131 <212> TYPE: DNA
 132 <213> ORGANISM: Artificial Sequence
 134 <220> FEATURE:
 135 <223> OTHER INFORMATION: large NcoI-XbaI vector fragment ligated to SEQ ID NO:10
 137 <400> SEQUENCE: 9
 138 catggccaac gcttgctcact actctcactt atggtgttca atgctttt 48
 141 <210> SEQ ID NO: 10

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142 <211> LENGTH: 48
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144 <213> ORGANISM: Artificial Sequence
146 <220> FEATURE:
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149 <400> SEQUENCE: 10
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154 <211> LENGTH: 36
155 <212> TYPE: DNA
156 <213> ORGANISM: Artificial Sequence
158 <220> FEATURE:
159 <223> OTHER INFORMATION: 5' primer based on pGFP-N1 plasmid
161 <400> SEQUENCE: 11
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166 <211> LENGTH: 35
167 <212> TYPE: DNA
168 <213> ORGANISM: Artificial Sequence
170 <220> FEATURE:
171 <223> OTHER INFORMATION: 3' primer based on pGFP-N1 plasmid
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177 <210> SEQ ID NO: 13
178 <211> LENGTH: 40
179 <212> TYPE: DNA
180 <213> ORGANISM: Artificial Sequence
182 <220> FEATURE:
183 <223> OTHER INFORMATION: 5' primer based on pZeoSV-LacZ plasmid
185 <400> SEQUENCE: 13
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189 <210> SEQ ID NO: 14
190 <211> LENGTH: 34
191 <212> TYPE: DNA
192 <213> ORGANISM: Artificial Sequence
194 <220> FEATURE:
195 <223> OTHER INFORMATION: 3' primer based on pZeoSV-LacZ plasmid
197 <400> SEQUENCE: 14
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201 <210> SEQ ID NO: 15
202 <211> LENGTH: 764
203 <212> TYPE: DNA
204 <213> ORGANISM: Aequorea Victoria
207 <220> FEATURE:
208 <221> NAME/KEY: CDS
209 <222> LOCATION: (8)..(721)
211 <400> SEQUENCE: 15
212 aagcttt atg agt aaa gga gaa gaa ctt ttc act gga gtt gtc cca att          49
213      Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile

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214          1          5          10
216 ctt gtt gaa tta gat ggc gat gtt aat ggg caa aaa ttc tct gtt agt      97
217 Leu Val Glu Leu Asp Gly Asp Val Asn Gly Gln Lys Phe Ser Val Ser
218 15          20          25          30
220 gga gag ggt gaa ggt gat gca aca tac gga aaa ctt acc ctt aaa ttt      145
221 Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe
222          35          40          45
224 att tgc act act ggg aag cta cct gtt cca tgg cca acg ctt gtc act      193
225 Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr
226          50          55          60
228 act ttc tct tat ggt gtt caa tgc ttt tca aga tac cca gat cat atg      241
229 Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met
230          65          70          75
232 aaa cag cat gac ttt ttc aag agt gcc atg ccc gaa ggt tat gta cag      289
233 Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln
234          80          85          90
236 gaa aga act ata ttt tac aaa gat gac ggg aac tac aag aca cgt gct      337
237 Glu Arg Thr Ile Phe Tyr Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala
238 95          100          105          110
240 gaa gtc aag ttt gaa ggt gat acc ctt gtt aat aga atc gag tta aaa      385
241 Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys
242          115          120          125
244 ggt att gat ttt aaa gaa gat gga aac att ctt gga cac aaa atg gaa      433
245 Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Met Glu
246          130          135          140
248 tac aac tat aac tca cat aat gta tac atc atg gca gac aaa cca aag      481
249 Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Pro Lys
250          145          150          155
252 aat gga atc aaa gtt aac ttc aaa att aga cac aac att aaa gat gga      529
253 Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Lys Asp Gly
254          160          165          170
256 agc gtt caa tta gca gac cat tat caa caa aat act cca att ggc gat      577
257 Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
258 175          180          185          190
260 ggc cct gtc ctt tta cca gac aac cat tac ctg tcc acg caa tct gcc      625
261 Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala
262          195          200          205
264 ctt tcc aaa gat ccc aac gaa aag aga gat cac atg atc ctt ctt gag      673
265 Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Ile Leu Leu Glu
266          210          215          220
268 ttt gta aca gct gct ggg att aca cat ggc atg gat gaa cta tac aaa      721
269 Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys
270          225          230          235
272 taaatgtcca gacttccaat tgacactaaa gggatccgaa ttc      764
275 <210> SEQ ID NO: 16
276 <211> LENGTH: 238
277 <212> TYPE: PRT
278 <213> ORGANISM: Aequorea Victoria
280 <400> SEQUENCE: 16

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282 Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
283 1 5 10 15
286 Glu Leu Asp Gly Asp Val Asn Gly Gln Lys Phe Ser Val Ser Gly Glu
287 20 25 30
290 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
291 35 40 45
294 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
295 50 55 60
298 Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln
299 65 70 75 80
302 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
303 85 90 95
306 Thr Ile Phe Tyr Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
307 100 105 110
310 Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
311 115 120 125
314 Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Met Glu Tyr Asn
315 130 135 140
318 Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Pro Lys Asn Gly
319 145 150 155 160
322 Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Lys Asp Gly Ser Val
323 165 170 175
326 Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
327 180 185 190
330 Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser
331 195 200 205
334 Lys Asp Pro Asn Glu Lys Arg Asp His Met Ile Leu Leu Glu Phe Val
335 210 215 220
338 Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys
339 225 230 235
342 <210> SEQ ID NO: 17
343 <211> LENGTH: 764
344 <212> TYPE: DNA
345 <213> ORGANISM: Aequorea victoria
348 <220> FEATURE:
349 <221> NAME/KEY: CDS
350 <222> LOCATION: (8)..(724)
352 <400> SEQUENCE: 17
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355 1 5 10
357 ctt gtt gaa tta gat ggc gat gtt aat ggg caa aaa ttc tcc gtt agt 97
358 Leu Val Glu Leu Asp Gly Asp Val Asn Gly Gln Lys Phe Ser Val Ser
359 15 20 25 30
361 gga gag ggt gaa ggt gat gca aca tac gga aaa ctt acc ctt aaa ttt 145
362 Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe
363 35 40 45
365 att tgc act act ggg aag cta cct gtt cca tgg cca acg ctt gtc act 193
366 Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr

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VERIFICATION SUMMARY

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